



SEQUENCE LISTING

<110> Reinherz, Ellis L.
Freund, Christian
Li, Jing
Nishizawa, Kazuhisa
Wagner, Gerhard

<120> Cloning and Characterization of a CD2
Binding Protein (CD2BP2)

<130> 1062.1021-004

<140> 09/873,106

<141> 2001-06-01

<150> US 60/111,007

<151> 1998-12-04

<150> US 60/115,647

<151> 1999-01-13

<150> PCT/US99/26993

<151> 1999-11-15

<160> 25

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)...(1143)

<400> 1

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tcttttttcc acctgcctt ccgcggattc ccagcttgag aaacacctct ttgccccgtc 120
atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag gat 168
Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
      1              5              10              15
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gag gat gaa atc att gtc ccc aag aag aag ctg gtg gac cct gtg gct 216
Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
      20              25              30
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ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264
Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
      35              40              45
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agc gat gag gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac	312
Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp	
50 55 60	
atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc	360
Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro	
65 70 75 80	
agc gag ggg ggt ggt cgg atc aca ccc ttt aac ctg cag gag gag atg	408
Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met	
85 90 95	
gag gaa ggc cac ttt gat gcc gat ggc aac tac ttc ctg aac cgg gat	456
Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp	
100 105 110	
gct cag atc cga gac agc tgg ctg gac aac att gac tgg gtg aag atc	504
Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile	
115 120 125	
cgg gag cgg cca cct ggc cag cgc cag gcc tca gac tcg gag gag gag	552
Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu	
130 135 140	
gac agc ttg ggc cag acc tca atg agt gcc caa gcc ctc ttg gag gga	600
Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly	
145 150 155 160	
ctt ttg gag ctc cta ttg cct aga gag aca gtg gct ggg gca ctg agg	648
Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg	
165 170 175	
cgt ctg ggg gcc cga gga gga ggc aaa ggg aga aag ggg cct ggg caa	696
Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln	
180 185 190	
ccc agt tcc cct cag cgc ctg gac cgg ctc tcc ggg ttg gcc gac cag	744
Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln	
195 200 205	
atg gtg gcc cgg ggc aac ctt ggt gtg tac cag gaa aca agg gaa cgg	792
Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg	
210 215 220	
ttg gct atg cgt ctg aag ggt ttg ggg tgt cag acc cta gga ccc cac	840
Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His	
225 230 235 240	
aat ccc aca ccc cca ccc tcc ctg gac atg ttc gct gag gag ttg gcg	888
Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala	
245 250 255	
gag gag gaa ctg gag acc cca acc cct acc cag aga gga gaa gca gag	936
Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu	
260 265 270	

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tcg cgg gga gat ggt ctg gtg gat gtg atg tgg gaa tat aag tgg gag 984
Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
      275                280                285

aac acg ggg gat gcc gag ctg tat ggg ccc ttc acc agc gcc cag atg 1032
Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
      290                295                300

cag acc tgg gtg agt gaa ggc tac ttc ccg gac ggt gtt tat tgc cgg 1080
Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
      305                310                315                320

aag ctg gac ccc cct ggt ggt cag ttc tac aac tcc aaa cgc att gac 1128
Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
      325                330                335

ttt gac ctc tac acc tgagcctgct gggggcccag tttggtgggc ctttctttcc 1183
Phe Asp Leu Tyr Thr
      340

tggactttgt ggaggaggca ccaagtgtct caggcagcga ggaaattgga ggccattttt 1243
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<210> 2

<211> 341

<212> PRT

<213> Homo sapiens

<400> 2

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 20      25      30
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 35      40      45
Ser Asp Glu Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
 50      55      60
Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
 65      70      75      80
Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
 85      90      95
Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
100     105     110
Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
115     120     125
Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
130     135     140
Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
145     150     155     160
Leu Leu Glu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
165     170     175
Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
180     185     190
Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
195     200     205
Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
210     215     220

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Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
 225 230 235 240
 Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
 245 250 255
 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
 260 265 270
 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
 275 280 285
 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
 290 295 300
 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
 305 310 315 320
 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
 325 330 335
 Phe Asp Leu Tyr Thr
 340

<210> 3
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 3
 Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr
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 Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly
 20 25

<210> 4
 <211> 27
 <212> PRT
 <213> Caenorhabditis elegans

<400> 4
 Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu
 1 5 10 15
 Phe Trp Leu Gln Ala Gly Tyr Phe Asn Asp Gly
 20 25

<210> 5
 <211> 27
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 <213> Caenorhabditis elegans

<400> 5
 Asp Pro Thr Glu Thr Arg Arg Gly Pro Phe Pro Lys Asp Gln Met Asn
 1 5 10 15
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 20 25

<210> 6
 <211> 27
 <212> PRT

<213> *Caenorhabditis elegans*

<400> 6

Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu
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20 25

<210> 7

<211> 29

<212> PRT

<213> *Saccharomyces cerevisiae*

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Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser
1 5 10 15
Gln Trp Tyr Ile Gly Gly Leu Glu Tyr Phe Ala Ser Thr
20 25

<210> 8

<211> 27

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser
1 5 10 15
Gln Trp Tyr Gln Gly Gly Tyr Phe Thr Pro Thr
20 25

<210> 9

<211> 17

<212> PRT

<213> Artificial Sequence

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<223> Motif in CD2 binding region of CD2BP2

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<222> 1,2,4,5,6,7,9,10,11,12,13,14,15

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 3

<223> Xaa can be Tyr or Phe

<221> VARIANT

<222> 8

<223> Xaa can be Met or Val

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<400> 9

Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Tyr
 1 5 10 15
 Phe

<210> 10

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> CD2BP2 binding region

<400> 10

Pro Pro Pro Gly His Arg
 1 5

<210> 11

<211> 70

<212> PRT

<213> Homo sapiens

<400> 11

Pro Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro
 1 5 10 15
 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro
 20 25 30
 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro
 35 40 45
 Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser
 50 55 60
 Leu Ser Pro Ser Ser Asn
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<210> 12

<211> 8

<212> DNA

<213> Artificial Sequence

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<223> Kozak consensus sequence

<400> 12

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8

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Flag Epitope

<400> 13
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<210> 14
<211> 8
<212> PRT
<213> Artificial Sequence

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<223> Flag Epitope

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<210> 15
<211> 31
<212> PRT
<213> Gallus gallus

<220>
<223> Flag Epitope

<400> 15
Trp Tyr Tyr Lys Asp Pro Gln Gly Glu Ile Gln Gly Pro Phe Ser Asn
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20 25 30

<210> 16
<211> 38
<212> PRT
<213> Drosophila melanogaster

<220>
<223> Flag Epitope

<400> 16
Glu Val Thr Trp Glu Phe Lys Trp Ser Gln Asp Glu Thr Asp Ile Gln
1 5 10 15
Gly Pro Phe Ser Thr Glu Lys Met Leu Lys Trp Ser Gln Glu Asn Thr
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Arg Tyr Phe Lys Asn Gly
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<210> 17
<211> 34
<212> PRT
<213> Leishmania major

<220>
<223> Flag Epitope

<400> 17

Val	Trp	Met	Met	Arg	Trp	Lys	Ala	Lys	Pro	Thr	Val	Gln	His	Gly	Pro
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Phe	Thr	Asp	Asp	Ala	Ile	Gln	Gln	Trp	Gly	Arg	Asp	Gly	Tyr	Phe	Gly
			20					25					30		
Lys	Lys														

<210> 18

<211> 36

<212> PRT

<213> *Caenorhabditis elegans*

<220>

<223> Flag Epitope

<400> 18

Val	Ile	Asp	Thr	Lys	Trp	His	Tyr	Leu	Gly	Pro	Asp	Ser	Glu	Lys	Tyr
1				5					10					15	
Gly	Pro	Tyr	Met	Ser	Lys	Asp	Met	Leu	Phe	Trp	Leu	Gln	Ala	Gly	Tyr
			20					25					30		
Phe	Asn	Asp	Gly												
			35												

<210> 19

<211> 35

<212> PRT

<213> *Caenorhabditis elegans*

<220>

<223> Flag Epitope

<400> 19

Val	Glu	Ser	Ser	Trp	Arg	Tyr	Ile	Asp	Thr	Gln	Gly	Gln	Ile	His	Gly
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Pro	Phe	Thr	Ile	Gln	Met	Met	Ser	Gln	Trp	Tyr	Ile	Gly	Gly	Tyr	Phe
			20					25					30		
Ala	Ser	Thr													
			35												

<210> 20

<211> 35

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<223> Flag Epitope

<400> 20

Ile	Glu	Ser	Gln	Trp	Lys	Tyr	Ile	Asp	Ser	Asn	Gly	Asn	Ile	Gln	Gly
1				5					10					15	
Pro	Phe	Gly	Thr	Asn	Asn	Met	Ser	Gln	Trp	Tyr	Gln	Gly	Gly	Tyr	Phe
			20					25					30		

Thr Pro Thr
35

<210> 21
<211> 31
<212> PRT
<213> Saccharomces pombe

<220>
<223> Flag Epitope

<400> 21
Trp Leu Tyr Lys Asp Pro Gln Asn Asn Val Gln Gly Pro Phe Thr Gly
1 5 10 15
Val Asp Met His Gln Trp Tyr Arg Ala Gly Tyr Phe Pro Leu Gly
20 25 30

<210> 22
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<223> Flag Epitope

<400> 22
Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro
1 5 10 15
Pro Pro Gly His Arg
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<210> 23
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<223> Flag Epitope

<400> 23
Asp Val Met Trp Glu Tyr Lys Trp Glu Asn Thr Gly Asp Ala Glu Leu
1 5 10 15
Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr Trp Val Ser Glu Gly
20 25 30
Tyr Phe Pro Asp Gly Val Tyr Cys Arg Lys Leu Asp Pro Pro Gly Gly
35 40 45
Gln Phe Tyr Asn Ser Lys Arg Ile Asp Phe Asp Leu Tyr Thr
50 55 60

<210> 24
<211> 31
<212> PRT
<213> Homo sapiens

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<220>

<223> Flag Epitope

<400> 24

Trp	Tyr	Tyr	Lys	Asp	Pro	Gln	Gly	Glu	Ile	Gln	Gly	Pro	Phe	Asn	Asn
1				5					10					15	
Gln	Glu	Met	Ala	Glu	Trp	Phe	Gln	Ala	Gly	Tyr	Phe	Thr	Met	Ser	
			20					25					30		

<210> 25

<211> 31

<212> PRT

<213> Homo sapiens

<220>

<223> Flag Epitope

<400> 25

Gln	Trp	Phe	Ser	Arg	Ser	Leu	Ala	Pro	Cys	Pro	Gly	Pro	Phe	Thr	Thr
1				5					10					15	
Gln	Glu	Met	Ala	Glu	Trp	Phe	Gln	Ala	Gly	Tyr	Phe	Ser	Met	Ser	
			20					25					30		

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):



- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: Sequences which lack a SEQ ID NO: tag are disclosed on pages 16, 19 and 20 of the specification. See attached Office Action

Applicant Must Provide: ONLY IF THE CRF DOES NOT CONTAIN SAID SEQUENCE.

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

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